

Figure 1

FAE1 w/ respect to time

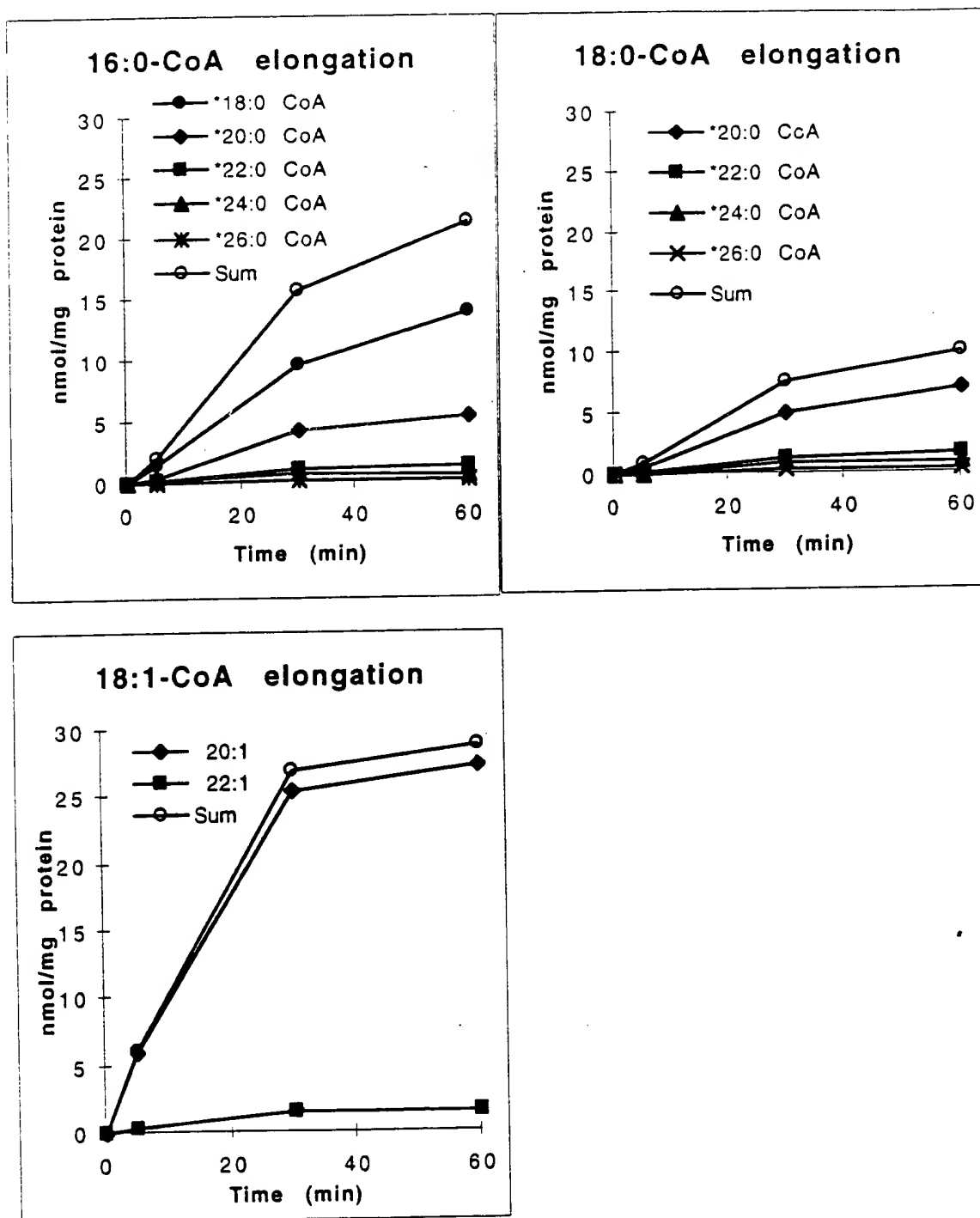
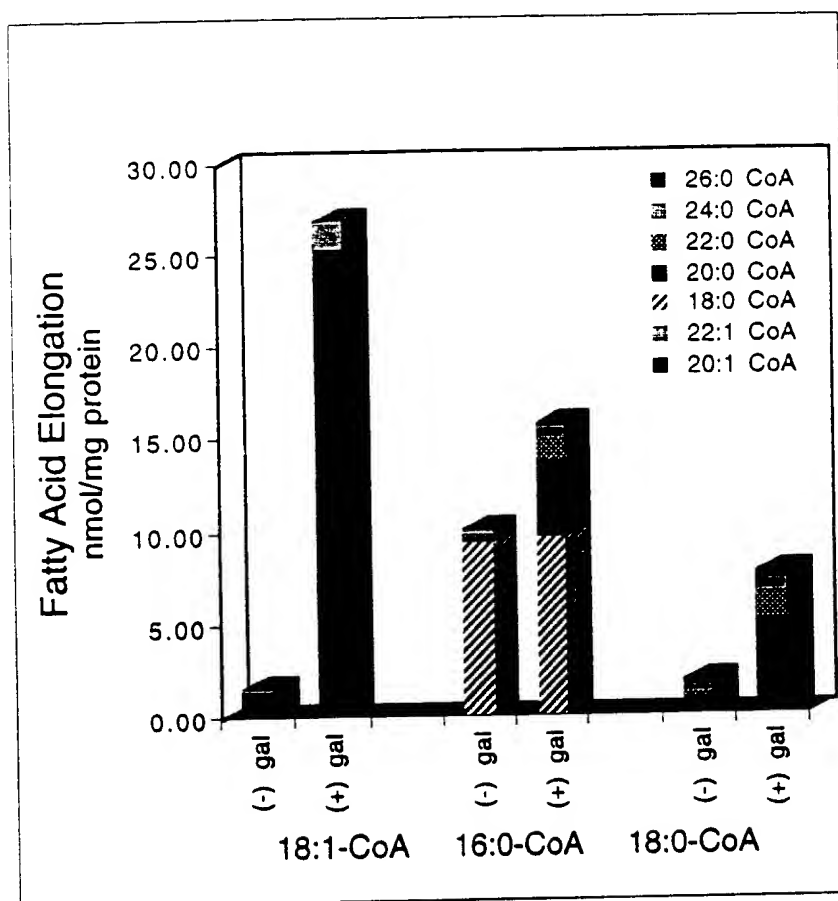


Figure 2



EL1 1560 bases

ATGGATCGAG	AGAGATTAAC	GGCGGAGATG	GCGTTTCGAG	ATTCATCATC	GGCCGTTATA
AGAATTCGAA	GACGTTTGCC	GGATTTATTA	ACGTCCGTTA	AGCTCAAATA	CGTGAAGCTT
GGACTTCACA	ACTCTTGCAA	CGTGACCACC	ATTCTCTTCT	TCTTAATTAT	TCTTCCTTTA
ACCGGAACCG	TGCTGGTTCA	GCTAACCGGT	CTAACGTTTCG	ATACGTTCTC	TGAGCTTTGG
TCTAACCAGG	CGGTTCAACT	CGACACGGCG	ACGAGACTTA	CCTGCTTGGT	TTTCTCTCTC
TTCGTTTTGA	CCCTCTACGT	GGCTAACCGG	TCTAAACCGG	TTTACCTAGT	GGATTTCTCC
TGCTACAAAC	CGGAAGACGA	GCGTAAAATA	TCAGTAGATT	CGTTCTTGAC	GATGACTGAG
GAAAATGGAT	CATTCAACGA	TGACACGGTT	CAGTTCAGC	AAAGAATCTC	GAACCGGGCC
GGTTTGGGAG	ACGAGACGTA	TCTGCCACGT	GGCATAACTT	CAACGCCCCC	GAAGCTAAAT
ATGTCAGAGG	CACGTGCCGA	AGCTGAAGCC	GTTATGTTTG	GAGCCTTAGA	TTCCCTCTTC
GAGAAAACCG	GAATTAAACC	GGCCGAAGTC	GGAATCTTGA	TAGTAAACTG	CAGCTTATTC
AATCCGACGC	CGTCTCTATC	AGCGATGATC	GTGAACCATT	ACAAGATGAG	AGAAGACATC
AAAAGTTACA	ACCTCGGAGG	AATGGGTTGC	TCCGCCGGAT	TAATCTCAAT	CGATCTCGCT
AACAATCTCC	TCAAAGCAAA	CCCTAATTCT	TACGCTGTCG	TGGTAAGCAC	GGAAAACATA
ACCCTAAACT	GGTACTTCGG	AAATGACCGG	TCAATGCTCC	TCTGCAACTG	CATCTTCCGA
ATGGGCGGAG	CTGCGATTCT	CCTCTCTAAC	CGCCGTCAAG	ACCGGAAGAA	GTCAAAGTAC
TCGCTGGTCA	ACGTCTGTCG	AACACATAAA	GGATCAGACG	ACAAGAATA	CAATTGCGTG
TACCAGAAGG	AAGACGAGAG	AGGAACAATC	GGTGTCTCTT	TAGCTAGAGA	GCTCATGTCT
GTCGCCGGAG	ACGCTCTGAA	AACAAACATC	ACGACTTTAG	GACCGATGGT	TCTTCCATTG
TCAGAGCAGT	TGATGTTCTT	GATTTCTTGG	GTCAAAGGA	AGATGTTCAA	GTTAAAAGTT
AAACCGTATA	TTCCGGATTT	CAAGCTAGCT	TTCGAGCATT	TCTGTATTCA	CGCAGGAGGT
AGAGCGGTTT	TAGACGAAGT	GCAGAAGAAT	CTTGATCTCA	AAGATTGGCA	CATGGAACCT
TCTAGAATGA	CTTTGCACAG	ATTTGGTAAC	ACTTCGAGTA	GCTCGCTTTG	GTATGAGATG
GCTTATACCG	AAGCTAAGGG	TCGGGTAAA	GCTGGTGACC	GACTTTGGCA	GATTGCGTTT
GGATCGGGTT	TCAAGTGTA	TAGTGCGGTT	TGGAAAGCGT	TACGACCGGT	TTCGACGGAG
GAGATGACCG	GTAATGCTTG	GGCTGGTTTCG	ATTGATCAAT	ATCCGGTTAA	AGTTGTGCAA

EL1
FIGURE 3

EL1 sequence
Molecular Weight 58379.00 Daltons
520 Amino Acids
62 Strongly Basic(+) Amino Acids (K,R)
52 Strongly Acidic(-) Amino Acids (D,E)
187 Hydrophobic Amino Acids (A,I,L,F,W,V)
144 Polar Amino Acids (N,C,Q,S,T,Y)
8.784 Isoelectric Point
10.804 Charge at PH 7.0

MDRERLTAEM	AFRDSSSAVI	RIRRRLPDLL	TSVKLKYVKL	GLHNSCNVTT	ILFFLIILPL
TGTVLVQLTG	LTFDTFSELW	SNQAVQLDTA	TRLTCLVFLS	FVLTLYVANR	SKPVYLVDFS
CYKPEDERKI	SVDSFLTMTTE	ENGSTDDTV	QFQQRISNRA	GLGDETYLPR	GITSTPPKLN
MSEARAEAEA	VMFGALDSLF	EKTGIKPAEV	GILIVNCSLF	NPTPSLSAMI	VNHYKMREDI
KSYNLGGMGC	SAGLISIDLA	NNLLKANPNS	YAVVVSTENI	TLNWYFGNDR	SMLLCNCIFR
MGGAAILLNS	RRQDRKKSKY	SLVNVVRTHK	GSDDKNYNVCV	YQKEDERGTI	GVSLARELMS
VAGDALKTNI	TTLGPMVLPL	SEQLMFLISL	VKRKMFKLKV	KPYIPDFKLA	FEHFCIHAGG
RAVLDEVQKN	LDLKDWHMEP	SRMTLHRFGN	TSSSSLWYEM	AYTEAKGRVK	AGDRLWQIAF
GSGFKCNSAV	WKALRPVSTE	EMTGNAWAGS	IDQYPVKVVQ		

FIGURE 4

58379.00

EL2 1479 bases

ATGGATTACC	CCATGAAGAA	GGTAAAAATC	TTTTTCAACT	ACCTCATGGC	GCATCGCTTC	
AAGCTCTGCT	TCTTACCATT	AATGGTTGCT	ATAGCCGTGG	AGGCGTCTCG	TCTTTCCACA	120
CAAGATCTCC	AAAACTTTTA	CCTCTACTTA	CAAAACAACC	ACACATCTCT	AACCATGTTT	
TTCCTTTACC	TCGCTCTCGG	GTGACTCTT	TACCTCATGA	CCCGGCCCAA	ACCCGTTTAT	240
CTCGTTGACT	TTAGCTGCTA	CCTCCCACCG	TCGCATCTCA	AAGCCAGCAC	CCAGAGGATC	
ATGCAACACG	TAAGGCTTGT	ACGAGAAGCA	GGCGCGTGGA	AGCAAGAGTC	CGATTACTTG	360
ATGGACTTCT	GCGAGAAGAT	TCTAGAACGT	TCCGGTCTAG	GCCAAGAGAC	GTACGTACCC	
GAAGGTCTTC	AAACTTTGCC	ACTACAACAG	AATTTGGCTG	TATCACGTAT	AGAGACGGAG	480
GAAGTTATTA	TTGGTGCGGT	CGATAATCTG	TTTCGCAACA	CGGAATAAG	CCCTAGTGAT	
ATAGGTATAT	TGGTGGTGAA	TTCAAGCACT	TTTAATCCAA	CACCTTCGCT	ATCAAGTATC	600
TTAGTGAATA	AGTTTAAACT	TAGGGATAAT	ATAAAGAGCT	TGAATCTTGG	TGGGATGGGG	
TGTAGCGCTG	GAGTCATCGC	TATCGATGCG	GCTAAGAGCT	TGTTACAAGT	TCATAGAAAC	720
ACTTATGCTC	TTGTGGTGAG	CACGGAGAAC	ATCACTCAAA	ACTTGTACAT	GGGTAACAAC	
AAATCAATGT	TGGTTACAAA	CTGTTTGTTC	CGTATAGGTG	GGGCCGCGAT	TTTGCTTTCT	840
AACCGGTCTA	TAGATCGTAA	ACGCGCAAAA	TACGAGCTTG	TTACACCGT	GCGGGTCCAT	
ACCGGAGCAG	ATGACCGATC	CTATGAATGT	GCAACTCAAG	AAGAGGATGA	AGATGGCATA	960
GTTGGGGTTT	CCTTGTCAAA	GAATCTACCA	ATGGTAGCTG	CAAGAACCCT	AAAGATCAAT	
ATCGCAACTT	TGGGTCCGCT	TGTTCTTCCC	ATAAGCGAGA	AGTTTCACTT	CTTTGTGAGG	1080
TTCGTTAAAA	AGAAGTTTCT	CAACCCCAAG	CTAAAGCATT	ACATTCCGGA	TTTCAAGCTC	
GCATTGAGC	ATTTCTGTAT	CCATGCGGGT	GGTAGAGCGC	TAATTGATGA	GATGGAGAAG	1200
AATCTTCATC	TAACCTCCACT	AGACGTTGAG	GCTTCAAGAA	TGACATTACA	CAGGTTTGGT	
AATACCTCTT	CGAGCTCCAT	TTGGTACGAG	TTGGCTTACA	CAGAAGCCAA	AGGAAGGATG	1320
ACGAAAGGAG	ATAGGATTTG	GCAGATTGCG	TTGGGGTCAG	GTTTTAAGTG	TAATAGTTCA	
GTTTGGGTGG	CTCTTCGTAA	CGTCAAGCCT	TCTACTAATA	ATCCTTGGA	ACAGTGTCTA	1440
CACAAATATC	CAGTTGAGAT	CGATATAGAT	TTAAAAGAG			

EL2
FIGURE 5

EL2 protein sequence
Molecular Weight 55799.30 Daltons
493 Amino Acids
55 Strongly Basic(+) Amino Acids (K,R)
46 Strongly Acidic(-) Amino Acids (D,E)
181 Hydrophobic Amino Acids (A,I,L,F,W,V)
134 Polar Amino Acids (N,C,Q,S,T,Y)
8.756 Isoelectric Point
10.995 Charge at PH 7.0

MDYPMKKVKI FFNYLMAHRF KLCFLPLMVA IAVEASRLST QDLQNFYLYL QNNHTSLTMF FLYLALGSTL
YLMTRPKPVY LVDFSCYLPP SHLKASTQRI MQHVRLVREA GAWKQESDYL MDFCEKILER SGLGQETYVP
EGLQTLPLQQ NLAVSRIETE EVIIGAVDNL FRNTGISPSD IGILVVNSST FNPTPSLSSI LVNKFKLRDN
IKSLNLGGMG CSAGVIAIDA AKSLLQVHRN TYALVVSTEN ITQONLYMGNN KSMLVTNCLF RIGGAAILLS
NRSIDRKRAK YELVHTVRVH TGADDRSYEC ATQEEDEDGI VGVSLSKNLP MVAARTLKIN IATLGPLVLP
ISEKFHFFVR FVKKKFLNPK LKHYIPDFKL AFEHFCIHAG GRALIDEMEK NLHLTPLDVE ASRMTLHRFG
NTSSSSIWYE LAYTEAKGRM TKGDRIWQIA LSGGFKCNSS VWVALRNVKP STNNPWEQCL HKYPVEIDID
LKE

FIGURE 6

EL3 protein sequence
Molecular Weight 56801.10 Daltons
504 Amino Acids
66 Strongly Basic(+) Amino Acids (K,R)
48 Strongly Acidic(-) Amino Acids (D,E)
183 Hydrophobic Amino Acids (A,I,L,F,W,V)
127 Polar Amino Acids (N,C,Q,S,T,Y)
9.315 Isoelectric Point
19.797 Charge at PH 7.0

LRQGR TKSKH LSKTICPTLR LSPMKNLKMW FFKILFISLM AGLAMKGSKI NVEDLQKFSL HHTQNNLQTI
SLLLFLVVFV WILYMLTRPK PVYLVD FSCY LPPSHLKVSI QTLMGHARRA REAGMCWKNK ESDHLVDFQE
KILERSGLGQ ETYIPEGLQC FPLQQGMGAS RKETEEVIFG ALDNLFRNTG VKPDDIGILV VNSSTFNPTP
SLASMIVNKY KLRDNIKSLN LGGMGCSAGV IAVDVAKGLL QVHRNTYAIV VSTENITQNL YLGKNK SMLV
TNCLFRVGGA AVLLSNRSD RNRKYELVH TVRIHTGSDD RSFECATQEE DEDGIIGVTL TKNLPMVAAR
TLKINIATLG PLVLPLKEKL AFFITFVKKK YFKPELRNYT PDFKLAFEHF CIHAGGRALI DELEKNLKLS
PLHVEASRMT LHRFGNTSSS SIWYELAYTE AKGRMKEGDR IWQIALGSGF KCNSSVWVAL RDVKPSANSP
WEDCMDRYPV EIDI

EL3
FIGURE 8

EL4 cDNA 1650 bases

ATGGGTAGAT	CCAACGAGCA	AGATCTGCTC	TCTACCGAGA	TCGTTAATCG	TGGGATCGAA	CCATCCGGTC
CTAACGCCGG	CTCACCAACG	TTCTCGGTTA	GGGTCAGGAG	ACGTTTGCCT	GATTTTCTTC	AGTCGGTGAA
CTTGAAGTAC	GTGAAACTTG	GTTACCACTA	CCTCATAAAC	CATGCGGTTT	ATTTGGCGAC	CATACCGGTT
CTTGTGCTGG	TTTTTAGTGC	TGAGGTTGGG	AGTTTAAGCA	GAGAAGAGAT	TTGGAAGAAG	CTTTGGGACT
ATGATCTTGC	AACTGTTATC	GGATTCTTCG	GTGTCTTTGT	TTTAACCGCT	TGTGTCTACT	TCATGTCTCG
TCCTCGCTCT	GTTTATCTTA	TTGATTTTCGC	TTGTTACAAG	CCCTCCGATG	AACACAAGGT	GACAAAAGAA
GAGTTCATAG	AACTAGCGAG	AAAATCAGGG	AAGTTCGACG	AAGAGACACT	CGGTTTCAAG	AAGAGGATCT
TACAAGCCTC	AGGCATAGGC	GACGAGACAT	ACGTCCCAAG	ATCCATCTCT	TCATCAGAAA	ACATAACAAC
GATGAAAGAA	GGTCGTGAAG	AAGCCTCTAC	AGTGATCTTT	GGAGCACTAG	ACGAACTCTT	CGAGAAGACA
CGTGTA AAC	CTAAAGACGT	TGGTGTCTTT	GTGGTTAACT	GTAGCATTTT	CAACCCGACA	CCGTCGTTGT
CCGCAATGGT	GATAAACCAT	TACAAGATGA	GAGGGAACAT	ACTTAGTTAC	AACCTTGGAG	GGATGGGATG
TTCCGGCTGGA	ATCATAGCTA	TTGATCTTGC	TCGTGACATG	CTTCAGTCTA	ACCCTAATAG	TTATGCTGTT
GTTGTGAGTA	CTGAGATGGT	TGGGTATAAT	TGGTACGTGG	GAAGTGACAA	GTCAATGGTT	ATACCTAATT
GTTTCTTTAG	GATGGGTTGT	TCTGCCGTTA	TGCTCTCTAA	CCGTCGTCGT	GACTTTCGCC	ATGCTAAGTA
CCGTCTCGAG	CACATTGTCC	GAACTCATAA	GGCTGCTGAC	GACCGTAGCT	TCAGGAGTGT	GTACCAGGAA
GAAGATGAAC	AAGGATTCAA	GGGGTTGAAG	ATAAGTAGAG	ACTTAATGGA	AGTTGGAGGT	GAAGCTCTCA
AGACAAACAT	CACTACCTTA	GGTCTCTTGT	TCCTACCTTT	CTCCGAGCAG	CTTCTCTTCT	TTGCTGCTTT
GGTCCGCCGA	ACATTCTCAC	CTGCTGCCAA	AACGTCCACA	ACCACTTCCT	TCTCTACTTC	CGCCACCGCA
AAAACCAATG	GAATCAAGTC	TTCCTCTTCC	GATCTGTCCA	AGCCATACAT	CCCGGACTAC	AAGCTCGCCT
TCGAGCATT	TTGCTTCCAC	GCGGCAAGCA	AAGTAGTGCT	TGAAGAGCTT	CAAAAGAATC	TAGGCTTGAG
TGAAGAGAAT	ATGGAGGCTT	CTAGGATGAC	ACTTCACAGG	TTTGGAAACA	CTTCTAGCAG	TGGAATCTGG
TATGAGTTGG	CTTACATGGA	GGCCAAGGAA	AGTGTTTCGT	GAGGCGATAG	GGTTTGGCAG	ATCGCTTTTCG
GTTCTGGTTT	TAAGTGTAAC	AGTGTGGTGT	GGAAGGCAAT	GAGGAAGGTG	AAGAAGCCAA	CCAGGAACAA
TCCTTGGGTG	GATTGCATCA	ACCGTTACCC	TGTGCCTCTC			

EL4
FIGURE 9

1500 bp

EL4 protein sequence
Molecular Weight 61953.80 Daltons
550 Amino Acids
71 Strongly Basic(+) Amino Acids (K,R)
58 Strongly Acidic(-) Amino Acids (D,E)
191 Hydrophobic Amino Acids (A,I,L,F,W,V)
147 Polar Amino Acids (N,C,Q,S,T,Y)
9.036 Isoelectric Point
14.349 Charge at PH 7.0

MGRSNEQDLL	STEIVNRGIE	PSGPNAGSPT	FSVRVRRRLP	DFLQSVNLKY	VKLGHYHLIN	HAVYLATIPV
LVLVFSAEVG	SLSREEIWKK	LWDYDLATVI	GFFGVFVLTA	CVYFMSRPRS	VYLIDFACYK	PSDEHKVTKE
EFIELARKSG	KFDEETLGFK	KRILQASGIG	DETYVPRIS	SSENITTMKE	GREEASTVIF	GALDELFEKT
RVKPKDVGV	VVNCISIFNPT	PSLSAMVINH	YKMRGNILSY	NLGGMGCSAG	IIAIDLARDM	LQSNPNYSYAV
VVSTEMVGYN	WYVGS DKSMV	IPNCFRRMGC	SAVMLSNRRR	DFRHAKYRLE	HIVRTHKAAD	DRSFRSVYQE
EDEQGFKGLK	ISRDLMEVGG	EALKTNITTL	GPLVLPFSEQ	LLFFAALVRR	TFSPA AKTST	TTSFSTSATA
KTNGIKSSSS	DLSKPYIPDY	KLAFEHFCFH	AASKVVLEEL	QKNLGLSEEN	MEASRMTLHR	FGNTSSSGIW
YELAYMEAKE	SVRRGDRVWQ	IAFGSGFKCN	SVVWKAMRKV	KKPTRNNPWV	DCINRYPVPL	

EL4
FIGURE 10

EL5 cDNA 1611 bases

TCGAGCTACG	TCAGGGCTTT	TATATGCACA	AATTCTCATA	AAGTTTTCAA	TTTTATTCCA	TTTTTCTCGG
AAGCCATGGA	AGCTGCTAAT	GAGCCTGTTA	ATGGCGGATC	CGTACAGATC	CGAACAGAGA	ACAACGAAAG
ACGAAAGCTT	CCTAATTTCT	TACAAAGCGT	CAACATGAAA	TACGTCAAGC	TAGGTTATCA	TTACCTCATT
ACTCATCTCT	TCAAGCTCTG	TTTGGTTCCA	TTAATGGCGG	TTTTAGTCAC	AGAGATCTCT	CGATTAACAA
CAGACGATCT	TTACCAGATT	TGGCTTCATC	TCCAATACAA	TCTCGTTGCT	TTTCATCTTC	TCTCTGCTTT
AGCTATCTTT	GGCTCCACCG	TTTACATCAT	GAGTCGTCCC	AGATCTGTTT	ATCTCGTTGA	TTACTCTTGT
TATCTTCCTC	CGGAGAGTCT	TCAGGTTAAG	TATCAGAAGT	TTATGGATCA	TTCTAAGTTG	ATTGAAGATT
TCAATGAGTC	ATCTTTAGAG	TTTCAGAGGA	AGATTCTTGA	ACGTTCTGGT	TTAGGAGAAG	AGACTTATCT
CCCTGAAGCT	TTACATTGTA	TCCCTCCGAG	GCCTACGATG	ATGGCGGCTC	GTGAGGAATC	TGAGCAGGTA
ATGTTTGGTG	CTCTTGATAA	GCTTTTTCGAG	AATACCAAGA	TTAACCCTAG	GGATATTGGT	GTGTTGGTTG
TGAATTGTAG	CTTGTTTAAT	CCTACACCTT	CGTTGTCAGC	TATGATTGTT	AACAAGTATA	AGCTTAGAGG
GAATGTTAAG	AGTTTTAACC	TTGGTGGGAT	GGGGTGTAGT	GCTGGTGTTA	TCTCTATCGA	TTTAGCTAAA
GATATGTTGC	AAGTTCATAG	GAATACTTAT	GCTGTTGTGG	TTAGTACTGA	GAACATTACT	CAGAATTGGT
ATTTTGGGAA	TAAGAAGGCT	ATGTTGATTC	CGAATTGTTT	GTTTCGTGTT	GGTGGTTCCG	CGATTTTGTT
GTCGAACAAG	GGGAAAGATC	GTAGACGGTC	TAAGTATAAG	CTTGTTTCATA	CCGTTAGGAC	TCATAAAGGA
GCTGTTGAGA	AGGCTTTCAA	CTGTGTTTAC	CAAGAGCAAG	ATGATAATGG	GAAGACCGGG	GTTTCGTTGT
CGAAAGATCT	TATGGCTATA	GCTGGGGAAG	CTCTTAAGGC	GAATATCACT	ACTTTAGGTC	CTTTGGTTCT
TCCTATAAGT	GAGCAGATTC	TGTTTTTCAT	GACTTTGGTT	ACGAAGAAAC	TGTTTAACTC	GAAGCTGAAG
CCGTATATTC	CGGATTTCAA	GCTTGCGTTT	GATCATTTCT	GTATCCATGC	TGGTGGTAGA	GCTGTGATTG
ATGAGCTTGA	GAAGAATCTG	CAGCTTTTCGC	AGACTCATGT	CGAGGCATCC	AGAATGACAC	TGCACAGATT
TGGAAACACT	TCTTCGAGCT	CGATTTGGTA	TGAACTGGCT	TACATAGAGG	CTAAAGGTAG	GATGAAGAAA
GGAAACCGGG	TTTGGCAGAT	TGCTTTTGGA	AGTGGGTTTA	AGTGTAACAG	TGCAGTTTGG	GTGGCTCTAA
ACAATGTCAA	GCCTTCGGTT	AGTAGTCCGT	GGGAACACTG	CATCGACCGA	TATCCGGTTA	AGCTCGACTT

C

EL5
FIGURE 11

09883797 "061601

[illegible]

EL5
FIGURE 12

EL6

1502 bases

TCTCCGACGATGCCTCAGGCACCGATGCCAGAGTTCTCTAGCTCGGTGAAGCTCAAGTACGTGAAACTTGGTTACCAA
TATTTGGTTAACCATTCTTTGAGTTTTCTTTTGATCCCGATCATGGCTATTGTGCGCGTTGAGCTTCTTCGGATGGGT
CCTGAAGAGATCCTTAATGTTTGGAAATCACTCCAGTTTGACCTAGTTTCAAGTTCTATGTTCTTCCTTCTTTGTCTC
TTCATCTCCACTGTTTACTTTCATGTCCAAGCCACGCACCATCTACCTCGTTGACTATTCTTGTGTACAAGCCACCTGTC
ACGTGTCGTGTCCCCTTCGCAACTTTTCATGGAACACTCTCGTTTGATCCTCAAGGACAAGCCTAAGAGCGTCCGAGTTC
CAAATGAGAATCCTTGAACGTTCTGGCCTCGGTGAGGAGACTTGTCTCCCTCCGGCTATTCAATTATATTCCTCCCA
CCAACCATGGACGCGGCTAGAAGCGAGGCTCAGATGGTTATCTTCGAGGCCATGGACGATCTTTTCAAGAAAACCGGT
CTTAAACCTAAAGACGTCGACATCCTTATCGTCAACTGCTCTCTTTTCTCTCCACACCATCGCTCTCAGCTATGGTC
ATCAACAAATATAAGCTTAGGAGTAATATCAAGAGCTTCAATCTTTGCGGGATGGGCTGCAGCGCGGGCTGATCTCA
GTTGATCTAGCCCGCGACTTGCTCCAAGTTCATCCCAATTCAAATGCAATCATCGTCAGCACGGAGATCATAAGCCT
AATTACTATCAAGGCAACGAGAGAGCCATGTTGTTACCCAATTGTCTCTTCCGCATGGGTGCGGCAGCCATACACATG
TCAAACCGCCGGTCTGACCGGTGGCGAGCCAAATACAAGCTTTCCACCTCGTCCGGACACACCGTGGCGCTGACGAC
AAGTCTTTCTACTGTGTCTACGAACAGGAAGACAAAGAAGGACACGTTGGCATCAACTTGTCCAAAGATCTCATGGCC
ATCGCCGGTGAAGCCCTCAAGGCAAACATCACCACAATAGGTCTTTGGTCTTACC GGCGT CAGAACAACCTCTCTTC
CTCACGTCCCTAATCGGACGTAAAACTTTCAACCCGAAATGGAAACCATACATACCGGATTTCAAGCTGGCCTTCGAA
CACTTTTGCATTACGCAGGAGGCAGAGCGGTGATCGACGAGCTCCAAAAGAATCTACAACATATCAGGAGAACACGTT
GAGGCCTCAAGAATGACACTACATCGTTTTGGTAACACGTCATCTTCATCGTTATGGTACGAGCTTAGCTACATCGAG
TCTAAAGGGAGAATGAGGAGAGGCGATCGCGTTTGGCAAATCGCGTTTGGGAGTGGTTTCAAGTGTAACCTCTGCCGTG
TGGAAGTGTAACCGTACGATTAAGACACCTAAGGACGACCATGGTCCGATTGTATCGACCGTTACCCTGTCTTTATT
CCCGAAGTTGTCAAACCTCTA

EL6

FIGURE 13

0903797 161604

EL6 protein sequence
Molecular Weight 56687.90 Daltons
500 Amino Acids
59 Strongly Basic(+) Amino Acids (K,R)
46 Strongly Acidic(-) Amino Acids (D,E)
182 Hydrophobic Amino Acids (A,I,L,F,W,V)
127 Polar Amino Acids (N,C,Q,S,T,Y)
8.909 Isoelectric Point
14.567 Charge at PH 7.0

SPTMPQAMP	EFSSSVKLKY	VKLGQYLVN	HFLSFLLIPI	MAIVAVELLR	MGPEEILNVW	NSLQFDLVQV
LCSSFFVIFI	STVYFMSKPR	TIYLVYSCY	KPPVTCRVPF	ATFMEHSRLI	LKDKPKSVEF	QMRILERSGL
GEETCLPPAI	HYIPTPTMD	AARSEAQMVI	FEAMDDLFFK	TGLKPKDVID	LIVNCSLFSP	TPSLSAMVIN
KYKLRSNIKS	FNLSGMGCSA	GLISVDLARD	LLQVHPNSNA	IIVSTEIITP	NYYQGNERAM	LLPNCLFRMG
AAAIHMSNRR	SDRWRAKYKL	SHLVRTHRGA	DDKSFYCVYE	QEDKEGHVGI	NLSKDLMAIA	GEALKANITT
IGPLVLPASE	QLLFLTSLIG	RKIFNPKWKP	YIPDFKLAFE	HFCIHAGGRA	VIDELQKNLQ	LSGHEVASR
MTLHRFGNTS	SSSLWYELSY	IESKGRMRRG	DRVWQIAFGS	GFKCNSAVWK	CNRTIKTPKD	GPWSDCIDRY
PVEIPEVVKL						

1548 bases

[illegible]

EL7
FIGURE 15

EL7 protein sequence
Molecular Weight 57848.80 Daltons
516 Amino Acids
59 Strongly Basic(+) Amino Acids (K,R)
48 Strongly Acidic(-) Amino Acids (D,E)
189 Hydrophobic Amino Acids (A,I,L,F,W,V)
131 Polar Amino Acids (N,C,Q,S,T,Y)
8.872 Isoelectric Point
12.792 Charge at PH 7.0

MDGAGESRLG	GDGGGDGSVG	VQIRQTRMLP	DFLQSVNLKY	VKLGYHYLIS	NLLTLCLFPL	AVVISVEASQ
MNPDDLKQLW	IHLQYNLVS	IICSAILVFG	LTVYVMTRPR	PVYLVDVFCY	LPPDHLKAPY	ARFMEHSRLT
GDFDDSALEF	QRKILERSGL	GEDTYVPEAM	HYVPPRISMA	AAREEAEQVM	FGALDNLFAN	TNVKPKDIGI
LVVNCSLFNP	TPSLSAMIVN	KYKLRGNIRS	YNLGGMGCSA	GVIADVLAKE	MLLVHRNTYA	VVVSTENITQ
NWYFGNKKSM	LIPNCLFRVG	GSAVLLSNKS	RDKRRSKYRL	VHVVRTHRGA	DDKAFCRVYQ	EQDDTGRTGV
SLSKDLMAIA	GETLKTNITT	LGPLVLPIS	QILFFMTLVV	KKLFNGKVVP	YIPDFKLAFE	HFCIHAGGRA
VIDELEKNLQ	LSPVHVEASR	MTLHRFGNTS	SSSIWYELAY	IEAKGRMRRG	NRVWQIAFGS	GFKCNSAIWE
ALRHVKPSNN	SPWEDCIDKY	PVTLSY				

EL7
FIGURE 16

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